

Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
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 Db 1261 ACAGGGGCTGAAGGGAAAGCAAGGCCTTGTGATCTTAGGGACAAACATTTCACCTCTC 1320

 Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
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 Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
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 Db 1381 ACACTTCTTGCATCTCTTATTCACTGCTTGACTTGCAAGTGCTGGTCCACAAGGACAG 1440

 Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
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 Db 1441 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGCCGGCCTCACTGTTCCA 1500

 Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
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 Db 1501 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGGCCTGCATCTAAACTCCTT 1560

 Qy 521 Ser 521
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 Db 1561 TCT 1563

RESULT 9

AF135484

LOCUS AF135484 1722 bp mRNA linear PLN 02-AUG-1999
DEFINITION Glycine max cytochrome P450 monooxygenase CYP93C1v2p (CYP93C1v2)
 mRNA, complete cds.
ACCESSION AF135484
VERSION AF135484.1 GI:5059123
KEYWORDS
SOURCE Glycine max.
ORGANISM Glycine max.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
REFERENCE 1 (bases 1 to 1722)
AUTHORS Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
TITLE Molecular characterization of the enzyme catalyzing the aryl
 migration reaction of isoflavanoid biosynthesis in soybean
JOURNAL Arch. Biochem. Biophys. 367 (1), 146-150 (1999)
MEDLINE 99306846
PUBMED 10375412
REFERENCE 2 (bases 1 to 1722)
AUTHORS Steele,C.L., Gijzen,M., Qutob,D. and Dixon,R.A.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1999) Plant Biology, Noble Foundation, 2510 Sam
 Noble Pkwy, Ardmore, OK 73402, USA
FEATURES Location/Qualifiers
source 1. .1722
 /organism="Glycine max"
 /db_xref="taxon:3847"
gene 1. .1722
 /gene="CYP93C1v2"
CDS 36. .1601

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/gene="CYP93C1v2"
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/note="The functional expression of this cDNA demonstrated
2-hydroxyisoflavanone synthase activity"
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AF022462; causes change of P to L (aa 140)"
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BASE COUNT 470 a 422 c 407 g 423 t
ORIGIN

Alignment Scores:

Pred. No.:	1.52e-259	Length:	1722
Score:	2267.00	Matches:	454
Percent Similarity:	87.14%	Conservative:	0
Best Local Similarity:	87.14%	Mismatches:	67
Query Match:	94.62%	Indels:	0
DB:	8	Gaps:	0

US-09-857-581-66 (1-521) x AF135484 (1-1722)

Qy	1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20	Leu	Leu
Db	36 ATGTTGCTTGAACTTGCACCTGGTTATTGGTTTGCGCTCTGTTCTGCACATTGCGTCCC 95		
Qy	21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40		

Db 96 ACACCCACTGCAAAATCAAAGCACTTCGCCATCTCCAAACCCACCAAGCCAAAGCCT 155
 Qy 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
 Db 156 CGTCTTCCCTTCATAGGACACCTTCATCTCTAAAAGACAAACTTCTCCACTACGCAC 215
 Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 Db 216 ATCGACCTCTCCAAAAAACATGGTCCCTATTCTCTACTTTGGCTCATGCCAACC 275
 Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 Db 276 GTTGTGCTCCACACCAGAATTGTTCAAGCTCTCCAAACGCAGGCAACTTCC 335
 Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
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 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
 Db 396 ATGGTTCCCTCGGACCTACTGGAAGTTCTGAGGAAGCTCATCATGAACGACCTCTC 455
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
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 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
 Db 516 AGGGTTATGGCCAAGGCGCAGAGGCACAGAAGCCCCTTGACTGACCGAGGAGCTCTG 575
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
 Db 576 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGCGAGGCTGAGGAGATCAGAGAC 635
 Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
 Db 636 ATCGCTCGCGAGGTTCTTAAGATCTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 695
 Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
 Db 696 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTGAACAAGTTC 755
 Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
 Db 756 GACCCTGCGTTGAAAGGGTCATCAAGAACGCGCGTGGAGATCGAGGAGAAAGAAC 815
 Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuGluPheAla 280
 Db 816 GGAGAGGTTGTTGAGGGTGAGGTCAAGCGGGTTTCTTGACACTTGCTTGAATTGCT 875
 Qy 281 GluAspGluThr***GluIleLysIleThrLys***IleLysGlyLeuValValAsp 300
 Db 876 GAGGATGAGACCATGGAGATCAAATCACCAAGGACACATCAAGGGTCTGTTGTCAC 935
 Qy 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
 Db 936 TTTTCTCGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGCATTGGCAGAAC 995

Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
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 Db 996 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTGGAAAG 1055
 Asp Arg
 Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
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 Thr
 Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
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 Db 1116 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAACAGTGT 1175
 Glu Trp Ile Leu
 Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
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 Db 1176 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTTCATGTATGGCAAGTA 1235
 Arg Pro
 Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
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 Db 1236 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCTGAGAGGTTCTAGAG 1295
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 Qy 421 Thr***AlaGluGlyGluAla***LeuAspLeuArgGly***HisPheGlnLeuLeu 440
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 Ala Asn Met
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 Db 1356 CCATTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTCGGGAATGGCA 1415
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 Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGln 480
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 Db 1416 ACACTTCTTGCATCTCTTATTCAAGTGCTCGACTTGCAAGTGCTGGTCCACAAGGACAG 1475
 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
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 Db 1476 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGGCCGGCTCACTGTTCCA 1535
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 Db 1536 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGCGTTGCATCTAAACTCCTT 1595
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 Db 1596 TCT 1598

RESULT 10
AF022462
LOCUS AF022462 1824 bp mRNA linear PLN 02-MAR-1999
DEFINITION Glycine max cytochrome P450 monooxygenase CYP93C1p (CYP93C1) mRNA, complete cds.
ACCESSION AF022462
VERSION AF022462.1 GI:2739005
KEYWORDS
SOURCE Glycine max.
ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots;

Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.

REFERENCE 1 (bases 1 to 1824)
 AUTHORS Siminszky, B., Corbin, F.T., Ward, E.R., Fleischmann, T.J. and Dewey, R.E.
 TITLE Expression of a soybean cytochrome P450 monooxygenase cDNA in yeast and tobacco enhances the metabolism of phenylurea herbicides
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1750-1755 (1999)
 MEDLINE 99145622
 PUBMED 9990096

REFERENCE 2 (bases 1 to 1824)
 AUTHORS Siminszky, B., Dewey, R.E. and Corbin, F.T.
 TITLE Direct Submission
 JOURNAL Submitted (04-SEP-1997) Crop Science, North Carolina State University, Box 7620, Raleigh, NC 27695, USA

FEATURES Location/Qualifiers
 source 1. .1824
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 CDS 54. .1619
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 KKRREIVRRRN
 GEVVEGEVSGVFLDTL
 LEFAEDETMEIKITKDHI
 EGLVVDF
 SAGTD
 STAVATEW
 ALAE
 INNP
 KVLE
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 YSVVGKDR
 LVDE
 VTQNL
 PYIRAI
 VKTFRM
 HPLP
 VVKRK
 CTEE
 CINGY
 VPEGAL
 ILFNVWQVGRDP
 KYWDRP
 SEFR
 PERFLET
 GAEG
 EAGPL
 DLRG
 QHFQ
 LLPF
 GSRR
 MCP
 GVNL
 LATSG
 MATLL
 ASL
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 GPQG
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 AGLTV
 PRAHS
 LVCV
 PLARIG
 VASK
 LLS"

BASE COUNT 497 a 448 c 416 g 463 t
 ORIGIN

Alignment Scores:

Pred. No.:	1.3e-257	Length:	1824
Score:	2251.00	Matches:	451
Percent Similarity:	86.76%	Conservative:	1
Best Local Similarity:	86.56%	Mismatches:	69
Query Match:	93.95%	Indels:	0
DB:	8	Gaps:	0

US-09-857-581-66 (1-521) x AF022462 (1-1824)

Qy	1	MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro	20		
Db	54	ATGTTGCTTGAACTTGCAC	TGGTTATTGGTTGGCTCTGTTCTGCAC	TGCGTCCC	113
Qy	21	ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro	40		

Db	114	ACACCCACTGAAAATCAAAGCACTCGCCATCTCCAAACCCACCAAGCCCCAAAGCCT	173
Qy	41	ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***	60
Db	174	CGTCTTCCCTTCATAGGACACCTTCATCTCTAAAAGACAAACTTCTCCACTACGCACTC	233
Qy	61	IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr	80
Db	234	ATCGACCTCTCCAAAAAACATGGTCCCTATTCTCTCTACTTTGGCTCCATGCCAACC	293
Qy	81	ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer	100
Db	294	GTTGTTGCCTCCACACCAGAATTGTTCAAGCTCTCCTCCAAACGCACGAGGCAACTTCC	353
Qy	101	Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla	120
Db	354	TTCAACACAAGGTTCCAACCTCAGCCATAAGACGCCTCACCTATGATAGCTCAGTGGCC	413
Qy	121	*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu	140
Db	414	ATGGTTCCCTTCGGACCTTACTGGAAAGTTCTGAGGACGCTCATCATGAACGACCTTCCC	473
Qy	141	AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu	160
Db	474	AACGCCACCACGTAAACAAGTTGAGGCCTTGAGGACCCAACAGACCCGCAAGTTCTT	533
Qy	161	Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu	180
Db	534	AGGGTTATGCCCAAGGCGCAGAGGCACAGAACAGCCCCTGACTTGACCGAGGAGCTCTG	593
Qy	181	LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp	200
Db	594	AAATGGACCAACAGCACCATCTCCATGATGATGCTGGCGAGGCTGAGGAGATCAGAGAC	653
Qy	201	IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro	220
Db	654	ATCGCTCGCGAGGTTCTTAAGATCTTGCGAATACAGCCTCACTGACTTCATCTGGCCA	713
Qy	221	LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe	240
Db	714	TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTGAACAAGTTC	773
Qy	241	AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn	260
Db	774	GACCCTGTCGTTGAAAGGGTCATCAAGAACGCGCCGTGAGATCGTAGGGAGAAAGAAC	833
Qy	261	GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla	280
Db	834	GGAGAGGTTGTTGAGGGTGAGGTCAAGGGGGTTTCCTGACACTTGCTGAATTGCT	893
Qy	281	GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp	300
Db	894	GAGGATGAGACCATGGAGATCAAATCACCAAGGACCACATCGAGGGTCTGTTGTCGAC	953
Qy	301	***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu	320
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Qy 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
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 Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
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 Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
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 Db 1194 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTCAATGTATGGCAAGTA 1253

 Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
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 Db 1254 GGAAGAGACCCCCAAATACTGGGACAGACCATCGGAGTTCCGTCTGAGAGGTTCTAGAG 1313

 Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
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 Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
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 Db 1374 CCATTGGGTCTGGGAGGAGAACATGTGCCCTGGAGTCAATCTGGCTACTCGGGAATGGCA 1433

 Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGln 480
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 Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
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 Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
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 Db 1554 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGCGTTGCATCTAAACTCCTT 1613

 Qy 521 Ser 521
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 Db 1614 TCT 1616

RESULT 11

AF195799

LOCUS AF195799 1824 bp mRNA linear PLN 16-FEB-2000
 DEFINITION Glycine max isoflavone synthase 2 (ifs2) mRNA, complete cds.
 ACCESSION AF195799
 VERSION AF195799.1 GI:6979521
 KEYWORDS
 SOURCE Glycine max.
 ORGANISM Glycine max.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

REFERENCE Glycine.
 AUTHORS 1 (bases 1 to 1824)
 Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and McGonigle,B.
 TITLE Identification and expression of isoflavone synthase, the key enzyme for biosynthesis of isoflavones in legumes
 JOURNAL Nat. Biotechnol. 18 (2), 208-212 (2000)
 MEDLINE 20124255
 PUBMED 10657130
 REFERENCE 2 (bases 1 to 1824)
 AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-1999) Nutrition and Health, DuPont, P.O. Box 80402, Wilmington, DE 19880-0402, USA
 FEATURES Location/Qualifiers
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 CDS 54. .1619
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 BASE COUNT 497 a 448 c 416 g 463 t
 ORIGIN

Alignment Scores:

Pred. No.: 1.3e-257 Length: 1824
Score: 2251.00 Matches: 451
Percent Similarity: 86.76% Conservative: 1
Best Local Similarity: 86.56% Mismatches: 69
Query Match: 93.95% Indels: 0
DB: 8 Gaps: 0

US-09-857-581-66 (1-521) x AF195799 (1-1824)

Qy	41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***	60
Db		
Qy	174 CGTCTTCCTTCATAGGACACCTTCATCTCTAAAGACAAACTCTCCACTACGCACTC	233
Qy	61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr	80
Db		
Qy	234 ATCGACCTCTCCAAAAACATGGTCCCTATTCTCTACTTTGGCTCCATGCCAACCC	293
Qy	81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer	100
Db		
Qy	294 GTTGTGCTCCACACCAGAATTGTTCAAGCTCTCCTCAAACGCACGAGGCAACTTCC	353
Qy	101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla	120
Db		
Qy	354 TTCAACACAAGGTTCAAACCTCAGCCATAAGACGCCACCTATGATAGCTCAGTGGCC	413
Qy	121 *****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu	140
Db		
Qy	414 ATGGTCTCCCTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC	473
Qy	141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu	160
Db		
Qy	474 AACGCCACCCTGTAAACAAGTTGAGGCCTTGAGGACCCAACAGACCCGCAAGTCCCTT	533
Qy	161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu	180
Db		
Qy	534 AGGGTTATGCCCAAGGCGCAGAGGCACAGAAGCCCCTGACTTGACCGAGGAGCTCTG	593
Qy	181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp	200
Db		
Qy	594 AAATGGACCAACAGCACCATCTCCATGATGATGCTGGCGAGGCTGAGGAGATCAGAGAC	653
Qy	201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro	220
Db		
Qy	654 ATCGCTCGAGGTTCTTAAGATCTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA	713
Qy	221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe	240
Db		
Qy	714 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTGAACAGTTC	773
Qy	241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn	260
Db		
Qy	774 GACCCTGTCGTTGAAAGGTCAAGAAGCGCCGTGAGATCGTGAGGAGGAGAAAGAAC	833
Qy	261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla	280
Db		
Qy	834 GGAGAGGTTGTTGAGGGTGAGGTCAAGCAGGGTTTCCTGACACTTGCTGAATTGCT	893
Qy	281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValValAsp	300
Db		
Qy	894 GAGGATGAGACCATGGAGATCAAATACCAAGGACCACATCGAGGGTCTGTTGTCGAC	953
Qy	301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu	320
Db		
Qy	954 TTTTCTGGCAGGAACAGACTCCACAGCGGTGGCAACAGAGTGGGCATTGGCAGAACTC	1013
Qy	321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys	340

Db 1014 ATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTGAGGAGGTCTACAGTGTGTGGAAAG 1073
 Qy 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
 Db 1074 GACAGACTTGTGGACGAAGTTGACACTCAAAACCTCCTTACATTAGAGCAATCGTGAAG 1133
 Qy 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
 Db 1134 GAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGT 1193
 Qy 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
 Db 1194 GAGATTAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTCAATGTATGGCAAGTA 1253
 Qy 401 Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
 Db 1254 GGAAGAGACCCCAAATACTGGGACAGACCATCGGAGTTCCGTCCCTGAGAGGTTCTAGAG 1313
 Qy 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 Db 1314 ACAGGGGCTGAAGGGGAAGCAGGGCCTTTGATCTTAGGGACAAACATTTCAACTTCTC 1373
 Qy 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
 Db 1374 CCATTGGGTCTGGGAGGAGAATGTGCCCTGGAGTCAATCTGGCTACTCGGAAATGGCA 1433
 Qy 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
 Db 1434 ACACTTCTTGCATCTCTTATTCAAGTGCTCGACTTGCAAGTGCTGGTCCACAAGGACAG 1493
 Qy 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
 Db 1494 ATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGGCCGGCTCACTGTTCCA 1553
 Qy 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
 Db 1554 AGGGCACATAGTCTTGTCTGTGTTCCACTTGCAAGGATCGCGTTGCATCTAAACTCCTT 1613
 Qy 521 Ser 521
 Db 1614 TCT 1616

RESULT 12

AF195819

LOCUS AF195819 1902 bp DNA linear PLN 23-MAR-2000
 DEFINITION Glycine max isoflavone synthase 2 (ifs2) gene, complete cds.
 ACCESSION AF195819
 VERSION AF195819.1 GI:7288454
 KEYWORDS
 SOURCE Glycine max.
 ORGANISM Glycine max.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (bases 1 to 1902)

AUTHORS Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and McGonigle,B.
 TITLE Identification and expression of isoflavone synthase, the key enzyme for biosynthesis of isoflavones in legumes
 JOURNAL Nat. Biotechnol. 18 (2), 208-212 (2000)
 MEDLINE 20124255
 PUBMED 10657130
 REFERENCE 2 (bases 1 to 1902)
 AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-1999) Nutrition and Health, DuPont, PO Box 80402, Wilmington, DE 19880-0402, USA
 FEATURES Location/Qualifiers
 source 1. .1902
 /organism="Glycine max"
 /db_xref="taxon:3847"
 gene 1. .1902
 /gene="ifs2"
 mRNA join(1. .948,1085. .1902)
 /gene="ifs2"
 /product="isoflavone synthase 2"
 CDS join(52. .948,1085. .1753)
 /gene="ifs2"
 /note="cytochrome P450"
 /codon_start=1
 /product="isoflavone synthase 2"
 /protein_id="AAF45143.1"
 /db_xref="GI:7288455"
 /translation="MLLEALGLLVLALFLHLRPTPTAKSKALRHLPPSPKPRLPF
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 TRFQTSAIRRLTYDSSVAMVPFGPYWKFRKLIMNDLPNATTVNKLRLRTQQTRKFL
 RVMAQGAEAQKPLDLTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFI
 WPLKHLKVGKYEKRIDDILNKFDPVVERVIKKREIVRRKNGEVVEGEVSGVFLDTL
 LEFAEDETMEIKITKDHEGLVVDFSAGTDSTAVATEWALAEINNPKVLEKAREEV
 YSVVGKDRLVDEVDTQNL PYIRAIKETFRMHPPVVKRKCTEECEINGYVPEGAL
 ILFNWWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDRLRGQHFQLLPFGSGRRMCP
 GVNLATSGMATLLASLIQCFDLQVLGPQGQILKGDAKVSMEERAGLTVPRAHSLVCV
 PLARIGVASKLILS"

BASE COUNT 517 a 455 c 440 g 490 t
 ORIGIN

Alignment Scores:

Pred. No.:	1.06e-251	Length:	1902
Score:	2201.50	Matches:	451
Percent Similarity:	79.72%	Conservative:	1
Best Local Similarity:	79.54%	Mismatches:	69
Query Match:	91.88%	Indels:	46
DB:	8	Gaps:	1

US-09-857-581-66 (1-521) x AF195819 (1-1902)

Qy	1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro	20
Db	52 ATGTTGCTTGAAC TTGCAC TTGGTT ATTGGTTTGGCTCTGTTCTGCACTTGCGTCCC	111
Qy	21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro	40

Db 112 ACACCCACTGAAAATCAAAGCACTTCGCCATCTCCAAACCCACCAAGCCAAAGCCT 171
 Qy 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 172 CGTCTTCCCTTCATAGGACACCTTCATCTCTAAAAGACAAACTCTCCACTACGCAC 231
 Qy 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 232 ATCGACCTCTCCAAAAAACATGGTCCCTATTCTCTCTACTTTGGCTCCATGCCAACC 291
 Qy 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
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 Db 292 GTTGTGCGCTCCACACCAGAATTGTTCAAGCTCTCCTCCAAACGCACGAGGCAACTTCC 351
 Qy 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 352 TTCAACACAAGGTTCAAACCTCAGCCATAAGACGCCACCTATGATAGCTCAGTGGCC 411
 Qy 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeu 140
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 Db 412 ATGGTTCCCTTCGGACCTTACTGGAAGTTCGTGAGGAAGCTCATCATGAACGACCTTCCC 471
 Qy 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
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 Db 472 AACGCCACCACTGTAAACAAGTTGAGGCCTTGAGGACCCAACAGACCCGCAAGTTCCCT 531
 Qy 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
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 Db 532 AGGGTTATGGCCAAGGCGCAGAGGCACAGAAGCCCCCTGACTGACCGAGGAGCTCTG 591
 Qy 181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluIleArgAsp 200
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 592 AAATGGACCAACAGCACCATCTCCATGATGATGCTCGCGAGGCTGAGGAGATCAGAGAC 651
 Qy 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
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 Db 652 ATCGCTCGCGAGGTTCTTAAGATCTTGGCGAATACAGCCTCACTGACTTCATCTGGCCA 711
 Qy 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
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 Db 712 TTGAAGCATCTCAAGGTTGGAAAGTATGAGAAGAGGATCGACGACATCTGAACAAGTT 771
 Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
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 Db 772 GACCCTGTCGTTGAAAGGGTCATCAAGAACCGCGTGGAGATCGTGGAGGAGAAAGAAC 831
 Qy 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 832 GGAGAGGTTGGAGGGTGAGGTCAGCGGGTTTCCTGACACTTGCTTGAATTGCGT 891
 Qy 281 GluAspGluThr***GluIleLysIleThrLys*****IleLysGlyLeuValVal--- 299
 ||||| ||||| ||||| ||||| ||||| ||||| : : |||||
 Db 892 GAGGATGAGACCATGGAGATCAAATCACCAAGGACCACATCGAGGGTCTGTTGCGT 951
 Qy 299 ----- 299
 Db 952 AGTTTCCTGCTTCATTGATCGAAATATGCAGTATTTGTTAACAGAGATCGAGAA 1011

Qy 299 -----
 Db 1012 TTGACATTATATTATGTGGTGGCAATTAATTAACGGTACGCATTCTTAATCGATAT 1071
 Qy 300 -----Asp***PheSerAlaGly***AspSerThrAla*****ThrGluTr 315
 ||||| ||||||| ||||| ||||| ||||| ||||| |||||
 Db 1072 TGTGTATGTGCAGGACTTTCTGGCAGGAACAGACTCCACAGCGTGCAACAGAGTG 1131
 Qy 315 pAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Ty 335
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1132 GGCATTGGCAGAACTCATCAACAATCCTAAGGTGTTGGAAAAGGCTCGTAGGGAGGTCTA 1191
 Qy 335 rSerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIl 355
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1192 CAGTGTGTTGGAAAGGACAGACTTGACGAGTTGACACTCAAAACCTTCCTTACAT 1251
 Qy 355 eArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLy 375
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 Db 1252 TAGAGCAATCGTGAAGGAGACATTCCGCATGCACCCGCCACTCCCAGTGGTCAAAAGAAA 1311
 Qy 375 sCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Ph 395
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1312 GTGCACAGAACAGACTGTGAGATTAAATGGATATGTGATCCCAGAGGGAGCATTGATTCTCTT 1371
 Qy 395 eAsnValTrpGlnValGly***Asp***LysTyrTrpAspArgProSerGlu***ArgPr 415
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 Db 1372 CAATGTATGGCAAGTAGGAAGAGACCCCCAAATACTGGACAGACCATCGGAGTTCCGTCC 1431
 Qy 415 oGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly** 435
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 Db 1432 TGAGAGGTTCCCTAGAGACAGGGCTGAAGGGAAAGCAGGGCCTTGTGATCTTAGGGACA 1491
 Qy 435 *HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAl 455
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 Db 1492 ACATTTCAACTCTCCCATTGGGTCTGGGAGGAGATGTGCCCTGGAGTCAATCTGGC 1551
 Qy 455 aThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLe 475
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 Db 1552 TACTTCGGGAATGGCAACACTTCTGCATCTTATTCAAGTGCTTCGACTTGCAAGTGCT 1611
 Qy 475 uGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAl 495
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 Db 1612 GGGTCCACAAGGACAGATATTGAAGGGTGGTGACGCCAAAGTTAGCATGGAAGAGAGAGC 1671
 Qy 495 aGlyLeuThrValProArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyVa 515
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 Db 1672 CGGCCTCACTGTTCCAAGGGCACATAGTCTGTGTTCCATTGCAAGGATCGCGT 1731
 Qy 515 lAlaSerLysLeuLeuSer 521
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 Db 1732 TGCATCTAAACTCCTTCT 1750

RESULT 13

AF195818

LOCUS AF195818 1800 bp DNA linear PLN 23-MAR-2000
 DEFINITION Glycine max isoflavone synthase 1 (ifs1) gene, partial cds.

ACCESSION AF195818
 VERSION AF195818.1 GI:7288452
 KEYWORDS
 SOURCE Glycine max.
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 REFERENCE 1 (bases 1 to 1800)
 AUTHORS Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and
 McGonigle,B.
 TITLE Identification and expression of isoflavone synthase, the key
 enzyme for biosynthesis of isoflavones in legumes
 JOURNAL Nat. Biotechnol. 18 (2), 208-212 (2000)
 MEDLINE 20124255
 PUBMED 10657130
 REFERENCE 2 (bases 1 to 1800)
 AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
 TITLE Direct Submission
 JOURNAL Submitted (18-OCT-1999) Nutrition and Health, DuPont, PO Box 80402,
 Wilmington, DE 19880-0402, USA
 FEATURES Location/Qualifiers
 source 1. .1800
 /organism="Glycine max"
 /db_xref="taxon:3847"
 gene <1. .>1800
 /gene="ifsl1"
 mRNA join(<1. .893,1112. .>1800)
 /gene="ifsl1"
 /product="isoflavone synthase 1"
 CDS join(<1. .893,1112. .1780)
 /gene="ifsl1"
 /note="cytochrome P450"
 /codon_start=3
 /product="isoflavone synthase 1"
 /protein_id="AAF45142.1"
 /db_xref="GI:7288453"
 /translation="LELALGLFVLALFLHLRPTPSAKSKALRHLNPSPKPRLPFIG
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 FQTSAIRRRTYDNSVAMVPFGPYWKFVRKLIMNDLLNATTVNKLRPLRTQQIRKFLRV
 MAQSAEAQKPLDVTEELLKWTNSTISMMMLGEAEEIRDIAREVLKIFGEYSLTDFIWP
 LKYLKVGYEKRIDDILNKFDPPVERVIKKRREIVRRRNQEVVEGEASGVFLDTLLE
 FAEDETMEIKITKEQIKGLVVDFFSAGTDSTAVATEWALAEINNPRVLQKAREEVYS
 VVGKDRLVDEVDTQNL PYIRAIKVETFRMHPPPLPVVKRKCTEECEINGYVPEGALVL
 FNVWQVGRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCPGV
 NLATSGMATLLASLIQCFDLQVLGPQGQILKGDDAKVSMEERAGLTVPRAHSLVCVPL
 ARIGVASKLLS".
 BASE COUNT 476 a 441 c 413 g 470 t
 ORIGIN

Alignment Scores:

Pred. No.:	3.04e-250	Length:	1800
Score:	2189.00	Matches:	451
Percent Similarity:	76.18%	Conservative:	0
Best Local Similarity:	76.18%	Mismatches:	68
Query Match:	91.36%	Indels:	74

DB :

8

Gaps :

1

US-09-857-581-66 (1-521) x AF195818 (1-1800)

Qy	3	LeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro	22
Db	3	CTGGAACTTGCACTTGGTTGTTGTAGCTTCTGCACTTGCCTCGTCCCACACCA	62
Qy	23	***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***ProArgLeu	42
Db	63	AGTGCAAAATCAAAGCACTTCGCCACCTCCAAACCCCTCCAAGGCCAAAGCCTCGTCTT	122
Qy	43	ProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAsp	62
Db	123	CCCTTCATTGGCACCTTCACCTCTAAAAGATAAACTCTCCACTATGCACTCATCGAT	182
Qy	63	LeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThrValVal	82
Db	183	CTCTCCAAAAGCATGGCCCTTATTCTCTCTCCCTCGGCTCCATGCCAACCGTCGTT	242
Qy	83	AlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***	102
Db	243	GCCTCCACCCCTGAGTTGTTCAAGCTCTCCCTCAAACCCACGAGGCAACTCCTTCAAC	302
Qy	103	ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla*****	122
Db	303	ACAAGGTTCCAAACCTCTGCCATAAGACGCCACTTACGACAACACTGTGGCCATGGTT	362
Qy	123	Pro***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeuLeuAsnAla	142
Db	363	CCATTGGACCTTACTGGAAGTTCTCGTGAGGAAGCTCATCATGAACGACCTCTAACGCC	422
Qy	143	ThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***	162
Db	423	ACCACCGTCAACAAGCTCAGGCCCTTGAGGACCCACAGATCCGAAGTCCCTTAGGGTT	482
Qy	163	MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeuLysTrp	182
Db	483	ATGGCCCAAAGCGCAGAGGCCAGAAGCCCTTGACGTCACCGAGGAGCTCTCAAATGG	542
Qy	183	***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAspIleAla	202
Db	543	ACCAACAGCACCATCTCCATGATGATGCTCGCGAGGCTGAGGAGATCAGAGACATCGCT	602
Qy	203	ArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys	222
Db	603	CGCGAGGTTCTTAAGATCTCGGCGAATACAGCCTCACTGACTCATCTGGCCTTGAAAG	662
Qy	223	***LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspPro	242
Db	663	TATCTCAAGGTTGGAAAGTATGAGAAGAGGATTGATGACATCTGAACAAGTTCGACCC	722
Qy	243	ValValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu	262
Db	723	GTCTGTTGAAAGGGTCATCAAGAACGCCGTGAGATCGTCAGAAGGAGAAAGAACGGAGAA	782
Qy	263	*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAsp	282

Db	783	GTTGTTGAGGGCGAGGCCAGCGCGTCTTCCTCGACACTTGCTTGAATTGCTGAGGAC	842
Qy	283	GluThr***GluIleLysIleThrLys*****IleLysGlyLeuValVal-----	299
Db	843	GAGACCATGGAGATCAAAATTACCAAGGAGCAAATCAAGGGCCTGTTGT-CGTAAGTTT	901
Qy	299	-----	299
Db	902	CCTTCTTCTCTCCTACTTATTACTTCTTCATTCATCATATGTATTGGCATTAAATAG	961
Qy	299	-----	299
Db	962	TATACTATATGAGAAAATATGTTACGCACTCACGGTGTAAAGATATGTGGTGTAAAAA	1021
Qy	299	-----	299
Db	1022	AAAAGAGATACAGAACAGTTGCTTTATGCATGTATGTTAACGTATTTACTCAAGTGGAA	1081
Qy	300	-----Asp***PheSerAlaGly***AspSerThr	309
Db	1082	ACTAATTAATTCTCAATTGGGTATGTAGGACTTTCTCTGCAGGGACAGATTCCACA	1141
Qy	310	Ala*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****	329
Db	1142	GCGGTGGCAACAGAGTGGCATTGGCAGAGCTCATCAACAATCCCAGGGTGTGCAAAAG	1201
Qy	330	AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThr	349
Db	1202	GCTCGTGAGGAGGTCTACAGTGTGGCAAGATAGACTCGTTGACGAAGTTGACACT	1261
Qy	350	GlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeu	369
Db	1262	CAAAACCTTCCTTACATTAGGCCATTGTGAAGGAGACATTCCGAATGCACCCACCACTC	1321
Qy	370	ProValValLysArgLysCys***GluGluCys***IleAsnGly***Val***ProGlu	389
Db	1322	CCAGTGGTCAAAAGAAAGTGCACAGAAGAGTGTGAGATTATGGGTATGTGATCCCAGAG	1381
Qy	390	GlyAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAspArg	409
Db	1382	GGAGCATTGGTTCTTCATGTTGGCAAGTAGGAAGGGACCCCAAATACTGGGACAGA	1441
Qy	410	ProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****	429
Db	1442	CCATCAGAATTCCGTCCCGAGAGGTTCTTAGAAACTGGTGTGAAGGGAAAGCAGGGCCT	1501
Qy	430	LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCys	449
Db	1502	CTTGATCTTAGGGGCCAGCATTCCAACCTCCCTCCATTGGGTCTGGGAGGAGAATGTGC	1561
Qy	450	ProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIleGlnCys	469
Db	1562	CCTGGTGTCAATTGGCTACTTCAGGAATGGCACACTTCTTGATCTTATCCAATGC	1621
Qy	470	PheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAlaLysVal	489

Db 1622 TTTGACCTGCAAGTGCTGGCCCTAAGGACAAATATTGAAAGGTGATGCCAAAGTT 1681
 Qy 490 SerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
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 Db 1682 AGCATGGAAAGAGAGAGCTGGCCTCACAGTTCCAAGGGCACATAGTCTCGTTGTGTTCCA 1741
 Qy 510 LeuAlaArgIleGlyValAlaSerLysLeuLeuSer 521
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 Db 1742 CTTGCAAGGATCGCGTTGCATCTAAACTCCTTTCT 1777

RESULT 14
AF195801
LOCUS AF195801 1501 bp mRNA linear PLN 16-FEB-2000
DEFINITION Medicago sativa isoflavone synthase 2 (ifs2) mRNA, partial cds.
ACCESSION AF195801
VERSION AF195801.1 GI:6979525
KEYWORDS
SOURCE Medicago sativa.
ORGANISM Medicago sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 1501)
AUTHORS Jung,W., Yu,O., Lau,S.M., O'Keefe,D.P., Odell,J., Fader,G. and McGonigle,B.
TITLE Identification and expression of isoflavone synthase, the key enzyme for biosynthesis of isoflavones in legumes
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REFERENCE 2 (bases 1 to 1501)
AUTHORS Jung,W., Yu,O., Odell,J., Fader,G. and McGonigle,B.
TITLE Direct Submission
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CDS	<1. .>1501 /gene="ifs2" /codon_start=3 /product="isoflavone synthase 2" /protein_id="AAF34522.1" /db_xref="GI:6979526" /translation="FLHLRPTPTAKSKALRHLNPSPKPRLPFIGHLHLLDKDLLHY ALIDLSSKKHGPLFSLYFGSMPTVVASTPELFKLFLQTHEATSFNTRFQTSAIRRLTYD SSVAMAPFGPYWKFRKLIMNDLLNATTVNKLRPLRTQQIRKFRLRVMQAQGAEAQKPLD LTEELLKWTNSTSMSMLGEAEEIRDIAREVLKIFGEYSLTDFIRPLKHLKVGYEKR IDDIILNKFDPVVERVIKKREIVRRKNGEVVEGEVSGVFLDTLLEFAEDETTEIKIT KDHIKGLVVDFFSAGTDSTAVATEWALAEINNPKVLEKAREEVYSSVGKDRLVDEVD TQNLPYIRAIKVETFRMHPPLPVVKRKCTEECEINGYVIPEGALILFNVWQVGRDSKY WDRPSEFRPERFLETGAEGEARPLDLRGQHFQLLPFGSGRRMCPGVNLATSGMATLLA SLIQCFDLQVLGPQGQILKGDAKVSMEERAGLTVPRAHSLVCVPLARIG"